

Thu Nov 18 16:38:24 2004

Search #3

seq1.rag

No body, the open ended w/ X goes page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:40 / Search time 67 seconds

(without alignments)
42.833 Million cell updates/sec

Title: SEQ1

Perfect score: 51
Sequence: 1 xcykwvct 8

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 356729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003s:*
- 7: Geneseq2004s:*
- 8: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	8	1	AAP61464
2	51	100.0	8	1	AAP71379
3	51	100.0	8	1	AAP71378
4	51	100.0	8	2	AAR07024
5	51	100.0	8	2	AAR07021
6	51	100.0	8	2	AAR07022
7	51	100.0	8	2	AAR05192
8	51	100.0	8	2	AAR14234
9	51	100.0	8	2	AAR14226
10	51	100.0	8	2	AAR10504
11	51	100.0	8	2	AAR26371
12	51	100.0	8	2	AAR26370
13	51	100.0	8	2	AAR27177
14	51	100.0	8	2	AAR27178
15	51	100.0	8	2	AAR27188
16	51	100.0	8	2	AAR27190
17	51	100.0	8	2	AAR23951
18	51	100.0	8	2	AAR40816
19	51	100.0	8	2	AAR41505
20	51	100.0	8	2	AAR41501
21	51	100.0	8	2	AAR31510
22	51	100.0	8	2	AAR42656
23	51	100.0	8	2	AAR56780
24	51	100.0	8	2	AAR56809
25	51	100.0	8	2	AAR56778

26	51	100.0	8	2	AAR56806
27	51	100.0	8	2	AAR55721
28	51	100.0	8	2	AAR50280
29	51	100.0	8	2	AAR85726
30	51	100.0	8	2	AAR76204
31	51	100.0	8	2	AAR85569
32	51	100.0	8	2	AAR85573
33	51	100.0	8	2	AAR81656
34	51	100.0	8	2	AAR81649
35	51	100.0	8	2	AAR92931
36	51	100.0	8	2	AAW48641
37	51	100.0	8	2	AAW18453
38	51	100.0	8	2	AAW68221
39	51	100.0	8	2	AAW6749
40	51	100.0	8	2	AAW50948
41	51	100.0	8	2	AAW51864
42	51	100.0	8	2	AAW51667
43	51	100.0	8	2	AAW51860
44	51	100.0	8	2	AAW22061
45	51	100.0	8	2	AAW22109

ALIGNMENTS

RESULT 1	
AAP61464	
ID AAP61464 standard; protein; 8 AA.	
XX	
AC AAP61464;	
XX	
DT 25-MAR-2003 (revised)	
DT 27-OCT-1991 (first entry)	
XX	
DE Cyclic octapeptide somatostatin analogue.	
XX	
KW Growth hormone; prolactin; insulin; glucagon; gastrin; secretin; Cholecystokinin.	
XX	
OS Synthetic.	
XX	
FH Key	Location/Qualifiers
FT Modified-site	1 /label= D-Phe
FT Disulfide-bond	2..7
FT Modified-site	4 /label= D-Trip
XX	
PN EP203031-A.	
XX	
PD 26-NOV-1986.	
XX	
PF 15-APR-1986; 86EP-00810174.	
XX	
PR 25-APR-1985; 85US-00727105.	
PR 28-MAR-1986; 86US-00843539.	
XX	
PA (TULANE) TULANE EDUCATIONAL FUND.	
XX	
PI Schally AV, Cai RZ;	
XX	
DR WPI, 1986-313466/48.	
XX	
PT New cyclic octapeptide somatostatin analogues - and reduced linear intermediates.	
XX	
PS Claim 8; Page 31; 33pp; English.	
XX	
CC Somatostatin analogues inhibit the release of growth hormone, prolactin, insulin, glucagon, gastrin, secretin and cholecystokinin. They also diminish gastrin stimulated secretion of gastric acid, and may be used in treatment of diabetic retinopathy, diabetes, ulcers, acute pancreatitis and agromegaly. The analogues may also be used in treating prostatic	

CC adeno-carcinomas, mammary carcinomas, insulinomas, gastrinomas and growth
 CC hormone and insulin dependent tumours. (Updated on 25-MAR-2003 to correct
 CC PA field.)
 CC
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYMKVCT 8
 :|||||
 Db 1 FCYMKVCT 8

RESULT 2
 AAP71378
 ID AAP71379 standard; peptide; 8 AA.
 XX
 AC AAP71379;

DT 09-SEP-2004 (revised)
 DT 25-MAR-2003 (revised)
 DT 03-OCT-2002 (revised)
 DT 03-MAY-1991 (first entry)

XX Sequence of somatostatin analogue.

XX Growth hormone secretion inhibitor; cancer therapy; Alzheimer's disease;
 KW diabetes.

XX Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 1 /label= pentafluoro-D-Phe

FT MISC-difference 4 /label= D-Trip

FT MISC-difference 8 /label= Thr-NH2

XX EP214872-A.

XX 18-MAR-1987.

XX 12-SEP-1986; 86EP-00307044.

XX 12-SEP-1985; 85US-00775488.

XX 17-JUN-1986; 86US-00875266.

XX 22-JUN-1988; 88US-00209883.

XX (TULANE) TULANE EDUCATIONAL FUND FUND.

XX Coy DH, Murphy WA, Heman ML;

XX WPI; 1987-074173/11.

XX Somatostatin analogue octa:peptide(s) with enhanced activity - are useful
 PT in the redn. of growth hormone, insulin glucagon, or pancreatic exocrine
 PT secretion, and have anticancer activity.

XX Disclosure; Page; 10pp; English.

XX Cpts. contg. the claimed peptides can be used instead of somatostatin.
 CC They are administered in somatostatin dosages or because of their greater
 CC potency in smaller dosages. Dosage is 0.01-1000 mcg./kg./day pref. 0.1-
 CC 100 mcg./kg./day to mammal eg human. (Updated on 03-OCT-2002 to add
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)

CC Revised record issued on 09-SEP-2004 : Correction to sequence location
 CC Sequence 8 AA;

Query Match 100.0%; Score 51; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYMKVCT 8
 :|||||
 Db 1 FCYMKVCT 8

RESULT 3
 AAP71378
 ID AAP71378 standard; peptide; 8 AA.
 XX
 AC AAP71378;

DT 09-SEP-2004 (revised)
 DT 25-MAR-2003 (revised)
 DT 03-OCT-2002 (revised)
 DT 03-MAY-1991 (first entry)

XX Sequence of somatostatin analogue.

XX Growth hormone secretion inhibitor; cancer therapy; Alzheimer's disease;
 KW diabetes.

XX Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 1 /label= D-beta-Nal

FT MISC-difference 4 /label= D-Trip

FT MISC-difference 8 /label= Thr-NH2

XX EP214872-A.

XX 18-MAR-1987.

XX 12-SEP-1986; 86EP-00307044.

XX 12-SEP-1985; 85US-00775488.

XX 17-JUN-1986; 86US-00875266.

XX 22-JUN-1988; 88US-00209883.

XX (TULANE) TULANE EDUCATIONAL FUND FUND.

XX Coy DH, Murphy WA, Heman ML;

XX WPI; 1987-074173/11.

XX Somatostatin analogue octa:peptide(s) with enhanced activity - are useful
 PT in the redn. of growth hormone, insulin glucagon, or pancreatic exocrine
 PT secretion, and have anticancer activity.

XX Disclosure; Page; 10pp; English.

XX Cpts. contg. the claimed peptides can be used instead of somatostatin.
 CC They are administered in somatostatin dosages or because of their greater
 CC potency in smaller dosages. Dosage is 0.01-1000 mcg./kg./day pref. 0.1-
 CC 100 mcg./kg./day to mammal eg human. (Updated on 03-OCT-2002 to add
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)

CC Revised record issued on 09-SEP-2004 : Correction to sequence location
 CC Sequence 8 AA;

Query Match 100.0%; Score 51; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 XCYWKVCT 8
DB      1 XCYWKVCT 8

RESULT 4
AAR07024
ID      AAR07024 standard; protein; 8 AA.
XX
AC      AAR07024;
XX
DT      21-JAN-1991 (first entry)
XX
DE      Octapeptide somatostatin analogue.
XX
KM      Growth hormone dependent cancer; diabetes; Alzheimers disease; Cirrhosis;
XX      hepatitis; insulin; glucagon.
XX
OS      Synthetic.
XX
FH      Key
FT      Modified-site      Location/Qualifiers
FT      /label= OTHER, Dextrorotatory
FT      /note= "N-Ac-D-beta-Nal"
FT      Modified-site      3
FT      /label= Iodinated phenyl ring
FT      Modified-site      4
FT      /label= Dextrorotatory
XX
PN      EP389180-A.
XX
PD      26-SEP-1990.
XX
PF      15-MAR-1990; 90EP-00302760.
XX
PR      15-MAR-1989; 89US-00323777.
XX
PA      (BIOM-) BIOMEASURE INC.
XX
PI      Eck CR, Moreau S;
XX
DR      WPI; 1990-292105/39.
XX
PT      New octa:peptide somatostatin analogues - useful for treating diabetes,
XX      liver disease, growth hormone dependent cancer, alzheimers disease etc.
XX
PS      Claim 5; Page 5; 8pp; English.
XX
CC      Analogues to somatostatin, useful for reducing or inhibiting release of
XX      antagonising growth hormone, insulin, glucagon or pancreatic exocrine
XX      solution. The peptides can treat diabetes related retinopathy, cirrhosis,
XX      hepatitis, Alzheimer's disease, cancers etc
XX
SQ      Sequence 8 AA;

Query Match      100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 XCYWKVCT 8
DB      1 XCYWKVCT 8

RESULT 5
AAR07021
ID      AAR07021 standard; protein; 8 AA.
XX
AC      AAR07021;
XX
DT      21-JAN-1991 (first entry)
XX
DE      Octapeptide somatostatin analogue.
XX

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XX      Growth hormone dependent cancer; diabetes; Alzheimers disease; Cirrhosis;
XX      hepatitis; insulin; glucagon.
XX
OS      Synthetic.
XX
FH      Key
FT      Modified-site      Location/Qualifiers
FT      /label= OTHER, Dextrorotatory
FT      /note= "D-beta-Nal"
FT      Modified-site      3
FT      /label= Iodinated phenyl ring
FT      Modified-site      4
FT      /label= Dextrorotatory
XX
PN      EP389180-A.
XX
PD      26-SEP-1990.
XX
PF      15-MAR-1990; 90EP-00302760.
XX
PR      15-MAR-1989; 89US-00323777.
XX
PA      (BIOM-) BIOMEASURE INC.
XX
PI      Eck CR, Moreau S;
XX
DR      WPI; 1990-292105/39.
XX
PT      New octa:peptide somatostatin analogues - useful for treating diabetes,
XX      liver disease, growth hormone dependent cancer, alzheimers disease etc.
XX
PS      Claim 5; Page 5; 8pp; English.
XX
CC      Analogues to somatostatin, useful for reducing or inhibiting release of
XX      antagonising growth hormone, insulin, glucagon or pancreatic exocrine
XX      solution. The peptides can treat diabetes related retinopathy, cirrhosis,
XX      hepatitis, Alzheimer's disease, cancers etc
XX
SQ      Sequence 8 AA;

Query Match      100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 XCYWKVCT 8
DB      1 XCYWKVCT 8

RESULT 6
AAR07022
ID      AAR07022 standard; protein; 8 AA.
XX
AC      AAR07022;
XX
DT      21-JAN-1991 (first entry)
XX
DE      Octapeptide somatostatin analogue.
XX
KM      Growth hormone dependent cancer; diabetes; Alzheimers disease; Cirrhosis;
XX      hepatitis; insulin; glucagon.
XX
OS      Synthetic.
XX
FH      Key
FT      Modified-site      Location/Qualifiers
FT      /label= Dextrorotatory
FT      /note= "Pentafluoro-D-Phe"
FT      Modified-site      3
FT      /label= Iodinated phenyl ring
FT      Modified-site      4
FT      /label= Dextrorotatory
XX

```


CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
:|||||
Db 1 FCYWKVCT 8

RESULT 9
AAR14226
ID AAR14226 standard; protein; 8 AA.

XX AAR14226;
AC
XX 25-MAR-2003 (revised)
DT 18-DEC-1991 (first entry)
DE Somatostatin deriv. #1 contg. cytotoxic moiety.
XX pituitary growth hormone; GH; antineoplastic.
KW Synthetic.

XX Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT /note= "4-Ibis(2-chloroethyl)amino]-Phe"
FT Disulfide-bond 2..7

XX EPA50480-A.

XX 09-OCT-1991.

XX 27-MAR-1991; 91EP-00104845.

XX 06-APR-1990; 90US-00505501.

XX (TULANE EDUCATIONAL FUND.
PA (SCHALL) SCHALL A V.

XX Schally AV, Janaky T, Cai RZ;
PI

XX WPI; 1991-297292/41.

XX New cyclic somatostatin peptide derivatives - have cytotoxic activity,
PT used for treating certain cancers e.g. adeno and mammary carcinoma(s),
PT gastric cancers, brain tumours, etc.

XX Claim 7; Page 9 and Page 27; 28pp; English.

XX The C-terminus is amidated. This peptide is an example of a generic
CC formula. It inhibits secretion of pituitary GH and has neoplastic effect.
CC It is useful for treatment of hormone-sensitive tumours. See AAR14225-
CC R14238. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
:|||||
Db 1 FCYWKVCT 8

RESULT 10
AAR10504

ID AAR10504 standard; protein; 8 AA.

XX AAR10504;

XX 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 09-APR-1991 (first entry)

XX Pamocate of somatostatin octapeptide.

XX Sustained release peptide compsn; lactic acid; glycolic acid;
KW somatostatin; luteinising hormone releasing hormone.

XX Unidentified.

XX Key Location/Qualifiers
FT Modified-site 1..1
FT /label= Phe= D-Phe
FT Disulfide-bond 2..7
FT Modified-site 4..4
FT /label= Trp= D-Trp

XX GB2234169-A.

XX 30-JAN-1991.

XX 17-JUL-1990; 90GB-00015722.

XX 28-JUL-1989; 89CH-00002829.

XX (DEBI-) DEBIOPHARM SA.

XX Orsolin P;

XX WPI; 1991-031530/05.

XX Sustained release pharmaceutical peptide compsn. prepn. - involves
PT preheating and compressing mixt. of lactic and glycolic acid copolymers
PT with active substance pamocate, etc.

XX Claim 9; Page 12; 14pp; English.

XX This peptide is used as the active substance in a pharmaceutical compsn.
CC for sustained release of somatostatin. It is mixed with a lactic
CC acid/glycolic acid co-polymer. All components are in the form of
CC microparticles and an injectable soln. is obt'd. See also AAR10501-03 and
CC AAR10505-09. (Updated on 10-MAR-2003 to add missing OS field.) (Updated
CC on 25-MAR-2003 to correct PA field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
:|||||
Db 1 FCYWKVCT 8

RESULT 11

ID AAR26371
AAR26371 standard; peptide; 8 AA.

XX AAR26371;

XX 25-MAR-2003 (revised)
DT 10-FEB-1993 (first entry)

XX Somatostatin analogue.

XX Skin disease; melanoma; keratosis; basal cell epithelial pagetoid;
KW basal cell carcinoma; non toxic.

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XX OS Synthetic.
XX XX
XX XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-beta-naphthylalanine"
XX FT Disulfide-bond 2. .7
XX FT Misc-difference 4
XX FT Modified-site 8 /note= "D-Trp"
XX FT /note= "amidated"
XX PN WO9213554-A1.
XX XX
XX PD 20-AUG-1992.
XX XX
XX PF 07-FEB-1992; 92WO-US001027.
XX XX
XX PR 08-FEB-1991; 91US-00652863.
XX XX
XX PA (BIOM-) BIOMEASURE INC.
XX XX
XX PI Bogden AE, Moreau J;
XX XX WPI, 1992-299754/36.
XX DR
XX XX
XX PT Anti-proliferative compsn. comprising somatostatin analogue - used to
XX PT treat benign and malignant proliferative skin diseases e.g. melanomas.
XX XX
XX PS Claim 10; Page 16; 25pp; English.
XX XX
XX CC The peptide is an example of a somatostatin analogue used to treat
XX CC melanomas and their malignant skin metastases (these express somatostatin
XX CC receptors), recurring keratosis, non-invasive basal cell epithelial
XX CC pagetoid and basal cell carcinoma. Peptides have 4 (pref. 6 or 7) amino
XX CC acids with at least 20 (pref. 50) percent homology with the core region
XX CC of somatostatin and has a D-Trp at position 4. See also AAR26367-74.
XX CC (Updated on 25-MAR-2003 to correct FN field.)
XX SQ
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 51; DB 2; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 XCYWKVCT 8
XX : |||||
XX 1 XCYWKVCT 8
XX
XX DB
XX
XX RESULT 12
XX AAR26370
XX ID AAR26370 standard; peptide; 8 AA.
XX XX
XX AC AAR26370;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 10-FEB-1993 (first entry)
XX XX
XX DE Somatostatin analogue.
XX XX
XX KW Skin disease; melanoma; keratosis; basal cell epithelial pagetoid;
XX KW basal cell carcinoma; non toxic.
XX XX
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-Phe"
XX FT Disulfide-bond 2. .7
XX FT Misc-difference 4 /note= "D-Trp"
XX FT Modified-site 8 /note= "D-Trp"
XX PF

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FT XX /note= "amidated"
FT PN WO9213554-A1.
FT XX
FT XX 20-AUG-1992.
FT PD
FT XX
FT PF 07-FEB-1992; 92WO-US001027.
FT XX
FT PR 08-FEB-1991; 91US-00652863.
FT XX
FT PA (BIOM-) BIOMEASURE INC.
FT XX
FT PI Bogden AE, Moreau J;
FT XX
FT DR WPI, 1992-299754/36.
FT XX
FT XX
FT PT Anti-proliferative compsn. comprising somatostatin analogue - used to
FT PT treat benign and malignant proliferative skin diseases e.g. melanomas.
FT XX
FT PS Claim 9; Page 15; 25pp; English.
FT XX
FT CC The peptide is an example of a somatostatin analogue used to treat
FT CC melanomas and their malignant skin metastases (these express somatostatin
FT CC receptors), recurring keratosis, non-invasive basal cell epithelial
FT CC pagetoid and basal cell carcinoma. Peptides have 4 (pref. 6 or 7) amino
FT CC acids with at least 20 (pref. 50) percent homology with the core region
FT CC of somatostatin and has a D-Trp at position 4. See also AAR26367-74.
FT CC (Updated on 25-MAR-2003 to correct FN field.)
FT XX
FT SQ
FT Sequence 8 AA;
FT
FT Query Match 100.0%; Score 51; DB 2; Length 8;
FT Best Local Similarity 87.5%; Pred. No. 1.7e+06;
FT Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
FT
FT QY 1 XCYWKVCT 8
FT : |||||
FT 1 FCYWKVCT 8
FT
FT DB
FT
FT RESULT 13
FT AAR27177
FT ID AAR27177 standard; peptide; 8 AA.
FT XX
FT AC AAR27177;
FT XX
FT DT 09-SEP-2004 (revised)
FT DT 25-MAR-2003 (revised)
FT DT 21-MAY-1998 (first entry)
FT XX
FT DE Somatostatin analogue tyrosine kinase inhibitor #1.
FT XX
FT KW tumour; cancer; neoplasm; malignancy; psoriasis; regulation of;
FT KW release of; growth hormone; insulin; glucagon; prolactin;
FT KW inhibit exopeptidase; inhibit tumour growth; tumour transformation.
FT XX
FT OS Synthetic.
FT XX
FT FH Key Location/Qualifiers
FT FT Modified-site 1 /note= "beta-aspartyl", where alpha-carboxy group forms
FT FT Disulfide-bond 2. .7 amide with indoline"
FT FT Misc-difference 4 /note= "D-form"
FT FT Modified-site 8 /note= "amidated"
FT FT
FT PN EP505680-A1.
FT XX
FT PD 30-SEP-1992.
FT XX
FT PF 27-JAN-1992; 92EP-00101196.

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XX PR 25-JAN-1991; 91HU-00000272.
XX PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
XX PI Keri G, Mezeo I, Horvath A, Vadasz Z, Tepian I, Balogh A;
XX PI Csuka O, Boekoenyi G, Szoeki B, Horvath J, Idei M, Seproedi J;
XX DR WPI; 1992-325051/40.
XX PT New octa:peptide or hepta:peptide somastatin analogues - as tyrosine
XX PT kinase inhibitors for treating tumours and psoriasis, and for regulating
XX PT hormone release.
XX PS Claim 5; Page 30; 36pp; English.
XX CC This peptide is a somatostatin analogue showing more advantageous and
XX CC selective pharmacological action than somatostatin. It has a structure
XX CC inhibiting the activity of exopeptidases. It can be used in medicaments
XX CC to inhibit tumour growth or the activity of tyrosine kinase enzymes
XX CC involved in tumour transformation. It is also useful for regulating the
XX CC release of growth hormone, insulin, glucagon and prolactin. It may also
XX CC be used to inhibit pathological processes such as psoriasis, elicited by
XX CC the pathological proliferation of skin cells. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX CC Revised record issued on 09-SEP-2004 : Correction to feature table key
XX SQ Sequence 8 AA;
XX SQ
XX Query Match 100.0%; Score 51; DB 2; Length 8;
XX Best Local Similarity 87.5%; Pred. No. 1.7e+06;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 XCYWKVCT 8
DB 1 DCYWKVCT 8

RESULT 14
AAR27178
ID AAR27178 standard; peptide; 8 AA.
XX AC AAR27178;
XX DT 09-SEP-2004 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1998 (first entry)
XX DE Somatostatin analogue tyrosine kinase inhibitor #2.
XX KW tumour; cancer; neoplasm; malignancy; psoriasis; regulation of;
XX KW release of; growth hormone; insulin; glucagon; prolactin;
XX KW inhibit exopeptidase; inhibit tumour growth; tumour transformation.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form"
XX FT Disulfide-bond 2. .7
XX FT Misc-difference 4 /note= "D-form"
XX FT Modified-site 8 /note= "amidated"
XX PN EP505680-A1.
XX PD 30-SEP-1992.
XX PF 27-JAN-1992; 92EP-00101196.
XX PR 25-JAN-1991; 91HU-00000272.

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XX PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
XX PI Keri G, Mezeo I, Horvath A, Vadasz Z, Tepian I, Balogh A;
XX PI Csuka O, Boekoenyi G, Szoeki B, Horvath J, Idei M, Seproedi J;
XX DR WPI; 1992-325051/40.
XX PT New octa:peptide or hepta:peptide somastatin analogues - as tyrosine
XX PT kinase inhibitors for treating tumours and psoriasis, and for regulating
XX PT hormone release.
XX PS Claim 5; Page 30; 36pp; English.
XX CC This peptide is a somatostatin analogue showing more advantageous and
XX CC selective pharmacological action than somatostatin. It has a structure
XX CC inhibiting the activity of exopeptidases. It can be used in medicaments
XX CC to inhibit tumour growth or the activity of tyrosine kinase enzymes
XX CC involved in tumour transformation. It is also useful for regulating the
XX CC release of growth hormone, insulin, glucagon and prolactin. It may also
XX CC be used to inhibit pathological processes such as psoriasis, elicited by
XX CC the pathological proliferation of skin cells. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX CC Revised record issued on 09-SEP-2004 : Correction to feature table key
XX SQ Sequence 8 AA;
XX SQ
XX Query Match 100.0%; Score 51; DB 2; Length 8;
XX Best Local Similarity 87.5%; Pred. No. 1.7e+06;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 XCYWKVCT 8
DB 1 FCYWKVCT 8

RESULT 15
AAR27188
ID AAR27188 standard; peptide; 8 AA.
XX AC AAR27188;
XX DT 09-SEP-2004 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1998 (first entry)
XX DE Somatostatin analogue tyrosine kinase inhibitor #12.
XX KW tumour; cancer; neoplasm; malignancy; psoriasis; regulation of;
XX KW release of; growth hormone; insulin; glucagon; prolactin;
XX KW inhibit exopeptidase; inhibit tumour growth; tumour transformation.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /label= OTHER
XX FT Misc-difference 4 /note= "D-tetrahydroisoquinoline carboxylic acid (D-Tric)"
XX FT Disulfide-bond 2. .7
XX FT Misc-difference 4 /note= "D-form"
XX FT Modified-site 8 /note= "amidated"
XX PN EP505680-A1.
XX PD 30-SEP-1992.
XX PF 27-JAN-1992; 92EP-00101196.
XX PR 25-JAN-1991; 91HU-00000272.

```

PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.

XX Keri G, Mezei I, Horvath A, Vadasz Z, Tepian I, Balogh A;
 PI Csuka O, Boekonyi G, Szoke B, Horvath J, Idei M, Szecedi J;
 XX WPI; 1992-325051/40.

DR New octa:peptide or hepta:peptide somastatin analogues - as tyrosine
 PT kinase inhibitors for treating tumours and psoriasis, and for regulating
 PT hormone release.

PS Example 11; Page 23; 36pp; English.

CC This peptide is a somatostatin analogue showing more advantageous and
 CC selective pharmacological action than somatostatin. It has a structure
 CC inhibiting the activity of exopeptidases. It can be used in medicaments
 CC to inhibit tumour growth or the activity of tyrosine kinase enzymes
 CC involved in tumour transformation. It is also useful for regulating the
 CC release of growth hormone, insulin, glucagon and prolactin. It may also
 CC be used to inhibit pathological processes such as psoriasis, elicited by
 CC the pathological proliferation of skin cells. (Updated on 25-MAR-2003 to
 CC correct PN field.)

CC Revised record issued on 09-SEP-2004 : Correction to feature table key

XX Sequence 8 AA;

Query Match 100.0%; Score 51; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
 |||||
 Db 1 XCYWKVCT 8

Search completed: November 18, 2004, 16:22:33
 Job time : 69 secs

Thu Nov 18 16:38:25 2004

seq1.rat

Two open

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:39 ; Search time 21 Seconds
(without alignments)
25.264 Million cell updates/sec

Title: SEQ1
Perfect score: 51
Sequence: 1 xcywkvct 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	8	1	US-08-266-748B-7
2	51	100.0	8	3	US-08-586-670A-13
3	51	100.0	8	3	US-08-586-670A-14
4	51	100.0	8	4	US-09-528-200-157
5	51	100.0	9	3	US-08-586-670A-11
6	51	100.0	9	3	US-08-586-670A-15
7	47	92.2	8	3	US-09-484-318-1
8	47	92.2	8	3	US-09-484-318-8
9	47	92.2	8	3	US-09-484-319-1
10	47	92.2	8	3	US-09-484-319-8
11	47	92.2	8	3	US-09-484-320-1
12	47	92.2	8	3	US-09-484-320-8
13	47	92.2	8	3	US-09-484-321-1
14	47	92.2	8	3	US-09-484-321-8
15	47	92.2	8	3	US-09-484-323-1
16	47	92.2	8	3	US-09-484-323-8
17	47	92.2	8	3	US-09-325-769-1
18	47	92.2	8	3	US-09-325-769-2
19	47	92.2	8	3	US-09-636-170-1
20	47	92.2	8	3	US-09-636-170-8
21	47	92.2	8	3	US-09-637-518-1
22	47	92.2	8	3	US-09-637-518-8
23	47	92.2	8	4	US-09-528-200-155
24	47	92.2	8	4	US-09-528-200-159
25	46	90.2	9	3	US-08-985-526-13
26	46	90.2	33	2	US-08-671-487A-3
27	46	90.2	33	4	US-09-194-296-3

28	46	90.2	34	3	US-08-985-526-15	Sequence 15, Appl
29	45	88.2	6	2	US-08-282-980B-8	Sequence 8, Appl
30	45	88.2	6	3	US-08-931-095-5	Sequence 5, Appl
31	45	88.2	6	4	US-09-528-200-195	Sequence 15, App
32	43	84.3	8	4	US-08-528-200-158	Sequence 15, App
33	43	84.3	8	3	US-08-586-670A-16	Sequence 16, Appl
34	41	80.4	8	3	US-08-586-670A-19	Sequence 19, Appl
35	41	80.4	5179	4	US-09-538-092-1258	Sequence 1258, Ap
36	39	76.5	386	4	US-09-252-991A-20390	Sequence 20390, A
37	38	74.5	195	4	US-09-270-767-45424	Sequence 45424, A
38	38	74.5	312	4	US-09-252-991A-18251	Sequence 18251, A
39	37	72.5	6	1	US-07-902-935-2	Sequence 2, Appl
40	37	72.5	6	2	US-08-465-764-3	Sequence 3, Appl
41	37	72.5	6	2	US-08-470-932-2	Sequence 2, Appl
42	37	72.5	6	2	US-08-467-025-2	Sequence 3, Appl
43	37	72.5	6	2	US-08-347-397-3	Sequence 22, Appl
44	37	72.5	6	3	US-08-931-095-22	Sequence 23, Appl
45	37	72.5	6	3	US-08-931-095-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-286-748B-7
Sequence 7, Application US/08286748B
Patent No. 5759542
GENERAL INFORMATION:
APPLICANT: Victor Gurevich
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,748B
FILING DATE: August 5, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: J. Peter Faase
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04547/013001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: Xaa is D-Naphthylalanine
US-08-286-748B-7
Query Match 100.0%; Score 51; Length 8;
Best Local Similarity Pred. No. 3.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XCYWKTCT 8
| | | | |
| | | | |
Db 1 XCYWKTCT 8

RESULT 2

US-08-586-670A-13
; Sequence 13, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBridge, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Xaa is D-naphthylalanine and is linked
; OTHER INFORMATION: to DTPA; Ttp is in the D conformation;
US-08-586-670A-13

Query Match 100.0%; Score 51; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XCYWKTCT 8
| | | | |
| | | | |
Db 1 XCYWKTCT 8

RESULT 3
US-08-586-670A-14
; Sequence 14, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBridge, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Xaa is D-naphthylalanine and is linked
; OTHER INFORMATION: to 2-ketoglutonyl; Ttp is in the D conformation;
US-08-586-670A-14

Query Match 100.0%; Score 51; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XCYWKTCT 8
| | | | |
| | | | |
Db 1 XCYWKTCT 8

RESULT 4
US-09-528-200-157
; Sequence 157, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHIA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGNER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 157
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence

Thu Nov 18 16:38:25 2004

seq1.rat

Page 3

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-528-200-157

Query Match 100.0%; Score 51; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 3.8e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 1 FCYWKVCT 8

RESULT 5

US-08-586-670A-11
Sequence 11, Application US/08586670A

Patent No. 6241965

GENERAL INFORMATION:

APPLICANT: McBride, William

APPLICANT: Dean, Richard T.

TITLE OF INVENTION: Somatostatin Derivatives

TITLE OF INVENTION: And their Radiolabeled Products

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Wilcoff, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/586,670A

FILING DATE: 22-APR-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 6241965nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,385-DD

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..3

OTHER INFORMATION: /label= Variant residues

OTHER INFORMATION: /note= "The Lys is linked to a BAT chelator

OTHER INFORMATION: through the side chain nitrogen; Xaa is

OTHER INFORMATION: D-naphthylalanine; the Cys sulfur is methylated;

FEATURE:

NAME/KEY: Modified-site

LOCATION: 5..8

OTHER INFORMATION: /label= Variant residues

OTHER INFORMATION: /note= "The Trp residue is in the D conformation;

OTHER INFORMATION: the Cys side chain sulfur is methylated;

US-08-586-670A-11

Query Match 100.0%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 2 XCYWKVCT 9

RESULT 6

US-08-586-670A-15

Sequence 15, Application US/08586670A

Patent No. 6241965

GENERAL INFORMATION:

APPLICANT: McBride, William

APPLICANT: Dean, Richard T.

TITLE OF INVENTION: Somatostatin Derivatives

TITLE OF INVENTION: And their Radiolabeled Products

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Wilcoff, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/586,670A

FILING DATE: 22-APR-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 6241965nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,385-DD

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..3

OTHER INFORMATION: /label= Variant residues

OTHER INFORMATION: /note= "Lys is linked to a BAT chelator

OTHER INFORMATION: through the side chain nitrogen and to DTPA

OTHER INFORMATION: at the N-terminus; Xaa is D-naphthylalanine;

OTHER INFORMATION: methylated;

OTHER INFORMATION: methylated;

OTHER INFORMATION: methylated;

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OTHER INFORMATION: methylated;

OTHER INFORMATION: methylated;

OTHER INFORMATION: methylated;

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/ Patent No. 6180085
/ GENERAL INFORMATION:
/ APPLICANT: Achilefu, Samuel
/ APPLICANT: Rajagopalan, Raghavan
/ APPLICANT: Dorshow, Richard B
/ APPLICANT: Bugaj, Joseph E.
/ TITLE OF INVENTION: NOVEL DYES
/ FILE REFERENCE: DNA STRING
/ CURRENT APPLICATION NUMBER: US/09/484,318
/ CURRENT FILING DATE: 2000-01-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Octreotide
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: This is D-phenylalanine
/ NAME/KEY: DISULFID
/ LOCATION: (2)..(7)
/ NAME/KEY: SITE
/ LOCATION: (4)
/ OTHER INFORMATION: This is D-tryptophan
/ NAME/KEY: SITE
/ LOCATION: (8)
/ OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-318-1
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Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db      1 FCYWKTC 8
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RESULT 8
US-09-484-318-8
/ Sequence 8, Application US/09484318
/ Patent No. 6180085
/ GENERAL INFORMATION:
/ APPLICANT: Achilefu, Samuel
/ APPLICANT: Rajagopalan, Raghavan
/ APPLICANT: Dorshow, Richard B
/ APPLICANT: Bugaj, Joseph E.
/ TITLE OF INVENTION: NOVEL DYES
/ FILE REFERENCE: DNA STRING
/ CURRENT APPLICATION NUMBER: US/09/484,318
/ CURRENT FILING DATE: 2000-01-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Octreotate
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: This is D-phenylalanine
/ NAME/KEY: DISULFID
/ LOCATION: (2)..(7)
/ NAME/KEY: SITE
/ LOCATION: (4)
/ OTHER INFORMATION: This is D-tryptophan
US-09-484-318-8
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Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy      1 XCYWKTCT 8
        :|||||
Db      1 FCYWKTC 8
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RESULT 9
US-09-484-319-1
/ Sequence 1, Application US/09484319
/ Patent No. 6180086
/ GENERAL INFORMATION:
/ APPLICANT: Achilefu, Samuel
/ APPLICANT: Rajagopalan, Raghavan
/ APPLICANT: Dorshow, Richard B
/ APPLICANT: Bugaj, Joseph E.
/ TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
/ FILE REFERENCE: DNA STRING
/ CURRENT APPLICATION NUMBER: US/09/484,319
/ CURRENT FILING DATE: 2000-01-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Octreotide
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: This is D-phenylalanine
/ NAME/KEY: DISULFID
/ LOCATION: (2)..(7)
/ NAME/KEY: SITE
/ LOCATION: (4)
/ OTHER INFORMATION: This is D-tryptophan
/ NAME/KEY: SITE
/ LOCATION: (8)
/ OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-319-1
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Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Oy      1 XCYWKTCT 8
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Db      1 FCYWKTC 8
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RESULT 10
US-09-484-319-8
/ Sequence 8, Application US/09484319
/ Patent No. 6180086
/ GENERAL INFORMATION:
/ APPLICANT: Achilefu, Samuel
/ APPLICANT: Rajagopalan, Raghavan
/ APPLICANT: Dorshow, Richard B
/ APPLICANT: Bugaj, Joseph E.
/ TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
/ FILE REFERENCE: DNA STRING
/ CURRENT APPLICATION NUMBER: US/09/484,319
/ CURRENT FILING DATE: 2000-01-18
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Octreotate
/ NAME/KEY: SITE
/ LOCATION: (1)
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```

OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
LOCATION: (2)..(7)
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan
US-09-484-319-8

```

```

Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 XCYWKTCT 8
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Db      1 FCYWKTCCT 8

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RESULT 11
US-09-484-320-1
Sequence 1, Application US/09484320
Patent No. 6180087
GENERAL INFORMATION:
APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorschow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
FILE REFERENCE: dnastring
CURRENT APPLICATION NUMBER: US/09/484,320
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Ooctrectide
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
LOCATION: (2)..(7)
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan
NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-320-1

```

```

Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 XCYWKTCT 8
       : |||||
Db      1 FCYWKTCCT 8

```

```

RESULT 12
US-09-484-320-8
Sequence 8, Application US/09484320
Patent No. 6180087
GENERAL INFORMATION:
APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorschow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
FILE REFERENCE: dnastring
CURRENT APPLICATION NUMBER: US/09/484,320
CURRENT FILING DATE: 2000-01-18

```

```

Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Ooctrectate
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
LOCATION: (2)..(7)
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan
US-09-484-320-8

```

```

Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e-05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 XCYWKTCT 8
       : |||||
Db      1 FCYWKTCCT 8

```

```

RESULT 13
US-09-484-321-1
Sequence 1, Application US/09484321
Patent No. 6183726
GENERAL INFORMATION:
APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorschow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
FILE REFERENCE: DNA STRING
CURRENT APPLICATION NUMBER: US/09/484,321
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Ooctrectide
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
LOCATION: (2)..(7)
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan
NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-321-1

```

```

Query Match          92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 XCYWKTCT 8
       : |||||
Db      1 FCYWKTCCT 8

```

```

RESULT 14
US-09-484-321-8
Sequence 8, Application US/09484321

```

Patent No. 6183726
GENERAL INFORMATION:
APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorschow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
FILE REFERENCE: DNA STRING
CURRENT APPLICATION NUMBER: US/09/484,321
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Octreotate
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
LOCATION: (2) .. (7)
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan
US-09-484-321-8

Query Match 92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. NO. 3.8e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XCYWKTCT 8
: |||||
Db 1 FCYWKTC 8

RESULT 15
US-09-484-323-1
Sequence 1, Application US/09484323
Patent No. 6190641
GENERAL INFORMATION:
APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorschow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: NOVEL INDOCYANINE DYES
FILE REFERENCE: DNA STRING
CURRENT APPLICATION NUMBER: US/09/484,323
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Octreotide
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
LOCATION: (2) .. (7)
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan
NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-323-1

Query Match 92.2%; Score 47; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. NO. 3.8e+05;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 XCYWKTCT 8
: |||||
Db 1 FCYWKTC 8

Search completed: November 18, 2004, 16:21:19
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:39 ; Search time 64 Seconds

(without alignments)
71.922 Million cell updates/sec

Title: SEQ1
Perfect score: 51
Sequence: 1 xcywkvct 8

Scoring table: BLOSUM62DX
Gapcp 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	86.3	468	2	Q81619
2	42	82.4	107	2	Q7PJB0
3	42	82.4	256	2	Q7R3E2
4	42	82.4	493	1	TNR8 RAT
5	42	82.4	498	1	TNR8 MOUSE
6	42	82.4	826	2	Q8B1U1
7	41	80.4	192	2	Q99GU2
8	41	80.4	192	2	Q9E228
9	41	80.4	192	2	Q91B09
10	41	80.4	192	2	Q8V5C5
11	41	80.4	312	2	Q81237
12	41	80.4	312	2	Q88982
13	41	80.4	317	2	Q8EVS5
14	41	80.4	322	2	Q8E219
15	41	80.4	338	2	Q8YFA7
16	41	80.4	338	2	Q8G2L2
17	41	80.4	622	2	Q7P1X6
18	41	80.4	5179	1	MUC2 HUMAN
19	40	78.4	117	2	Q6G3K0
20	40	78.4	405	2	Q6FRA0
21	40	78.4	475	2	Q9UAT5
22	40	78.4	593	2	Q6TLC6
23	40	78.4	593	2	AAQ96728
24	40	78.4	646	2	Q6TLC7
25	40	78.4	646	2	AAQ96727
26	40	78.4	821	2	Q956D4
27	39	76.5	310	2	Q8PK92
28	39	76.5	313	2	Q8PE59
29	39	76.5	315	2	Q706P3
30	39	76.5	315	2	CAE92907
31	39	76.5	316	2	Q8GQ67

32	39	76.5	323	2	Q8KMR0
33	39	76.5	324	2	Q6D9N8
34	39	76.5	358	2	Q6GR30
35	39	76.5	452	2	Q8CGA0
36	39	76.5	743	2	Q7N288
37	38	74.5	31	2	Q9DEW1
38	38	74.5	381	2	Q7CMF4
39	38	74.5	381	2	Q9X356
40	38	74.5	381	2	AAT28858
41	38	74.5	435	2	Q8N117
42	38	74.5	515	2	Q7WY59
43	38	74.5	767	2	Q7ZVU7
44	38	74.5	767	2	Q6TNV9
45	38	74.5	767	2	AAQ91220

ALIGNMENTS

```

RESULT 1
ID      Q81619      PRELIMINARY:      PRT:      468 AA.
AC      Q81619;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE      Zic family transcription factor.
OS      Name=HrzicN;
OC      Halocynthia roretzi (Sea squirt).
OC      Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC      Stolidobranchia; Pyridae; Halocynthia.
OX      NCBI_TaxID=7729;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22308874; PubMed=12421701;
RA      Wada S, Saiga H;
RT      "HrzicN, a new Zic family gene of ascidians, plays essential roles in
RL      the neural tube and notochord development.";
DR      EMBL; AB092643; BAC23063.1; -.
DR      HSSP; P08047; ISP2.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0003676; F:nucleic acid binding; IEA.
DR      GO; GO:0008270; F:zinc ion binding; IEA.
DR      InterPro; IPR007087; ZnF_C2H2.
DR      Pfam; PF00096; ZF_C2H2_4.
DR      ProDom; PD000003; ZnF_C2H2_1.
DR      SMART; SM00355; ZnF_C2H2_5.
DR      PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR      PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
SQ      SEQUENCE 468 AA; 51632 MW; DBB567B4A5C1FP31 CRC64;

Query Match      86.3%; Score 44; DB 2; Length 468;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 XCYWKVCT 8
Db      157 TCYWKDCT 164

RESULT 2
ID      Q7PJB0      PRELIMINARY:      PRT:      107 AA.
AC      Q7PJB0;
DT      01-MAR-2004 (TrEMBLrel. 26, Created)
DT      01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      ENSANGP0000024086.
GN      Name=ENSANGP0000020752;
OC      Anopheles gambiae str. PEET.
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

```

```

OK NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA801008964; EAA43862.1; -
SQ SEQUENCE 107 AA; 11827 MW; EC7388D611F12DE5 CRC64;

Query Match      82.4%; Score 42; DB 2; Length 107;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
DB 62 DCFWKVC 68

RESULT 3
QY QY3E2 PRELIMINARY; PRT; 256 AA.
AC QY3E2;
DT 01-MAR-2004 (TREMBlrel. 26 Created)
DT 01-MAR-2004 (TREMBlrel. 26 Last sequence update)
DE GLP_111_2064_2834.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000016; EAA41776.1; -
SQ SEQUENCE 256 AA; 27273 MW; AFB91EA48E9157A CRC64;

Query Match      82.4%; Score 42; DB 2; Length 256;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
DB 52 LCYWVC 58

RESULT 4
TNR8 RAT STANDARD; PRT; 493 AA.
AC P97525;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 8 precursor (CD30L
DE receptor) (Lymphocyte activation antigen CD30).
GN Name=TNfrsf8; Synonyms=CD30;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WRHA; TISSUE=T-cell lymphoma;
RX MEDLINE=97136705; PubMed=8982082;
RA Alzawa S., Satoh H., Horie R., Ito K., Choi S.H., Takeuchi H.,

```

```

RA Matnabe T.;
RT "Cloning and characterization of a cDNA for rat CD30 homolog and
RT chromosomal assignment of the genomic gene.";
RL Gene 182:155-162(1996).
CC -!- FUNCTION: Receptor for TNFSF8/CD30L. May play a role in the
CC regulation of cellular growth and transformation of activated
CC lymphoblasts. Regulates gene expression through activation of NF-
CC kappa-B (By similarity).
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3 and TRAF5 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Very low level of expression. Detected in
CC spleen, thymus and lung. Highly expressed in HttV-1 infected T-
CC cell lines.
CC -!- INDUCTION: By phytohemagglutinin (PHA) in spleen T-cells.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D42117; BAA07693.1; -
DR PIR; JCS486; JCS486.
DR HSSP; Q92956; JUMA.
DR RGD; 3879; Tnfrsf8.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 18
FT CHAIN 19 493
FT FT 19 493
FT FT 19 493
FT DOMAIN 19 255
FT TRANSMEM 256 276
FT DOMAIN 277 493
FT REPEAT 28 66
FT REPEAT 68 106
FT REPEAT 107 150
FT DISULFID 29 44
FT DISULFID 45 58
FT DISULFID 84 97
FT DISULFID 87 105
FT DISULFID 107 121
FT DISULFID 124 142
FT CARBOHYD 152 152
FT CARBOHYD 179 179
FT CARBOHYD 225 225
SQ SEQUENCE 493 AA; 52658 MW; 40B7503B3CB7C CRC64;

Query Match      82.4%; Score 42; DB 1; Length 493;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
DB 303 LCYWVC 309

RESULT 5
TNR8 MOUSE STANDARD; PRT; 498 AA.
AC Q60846;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 8 precursor (CD30L
DE receptor) (Lymphocyte activation antigen CD30).

```

```

GN Name=Thrsf8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=splenic;
RX MEDLINE=96132967; PubMed=6543792;
RA Bowen M.A., Lee R.K., Mireglia G., Nam S.Y., Podack E.R.;
RT "Structure and expression of murine CD30 and its role in cytokine
production."
RL J. Immunol. 156:442-449 (1996).
CC -1- FUNCTION: Receptor for TNFSF8/CD30L. May play a role in the
CC regulation of cellular growth and transformation of activated
CC lymphoblasts. Regulates gene expression through activation of NF-
CC kappa-B (By similarity).
CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3 and TRAF5 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Detected in thymus and in activated
CC splenocytes.
CC -1- INDUCTION: By concanavalin A and pokeweed mitogen in splenocytes.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U25416; AAA92887.1; -.
CC MGD: MGI:39908; Thrsf8.
CC InterPro: IPR001368; TNFR_C6.
CC Pfam: PF00207; TNFR_C6; 3.
CC SMART: SM00208; TNFR_3.
CC PROSITE: PS00652; TNFR_NGFR_1; 1.
CC PROSITE: PS00652; TNFR_NGFR_2; 2.
CC KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 18
FT CHAIN 19 498
FT FT 19 498
FT DOMAIN 19 258
FT TRANSMEM 259 279
FT DOMAIN 280 498
FT REPEAT 28 66
FT REPEAT 68 106
FT REPEAT 107 150
FT DISULFID 29 44
FT DISULFID 45 58
FT DISULFID 48 65
FT DISULFID 69 81
FT DISULFID 84 97
FT DISULFID 107 121
FT DISULFID 128 146
FT CARBOHYD 156 156
FT CARBOHYD 183 183
FT CARBOHYD 229 229
SQ SEQUENCE 498 AA; 53216 MW; 98CA2A05B38AFA71 CRC64;

```

```

Query Match      82.4%; Score 42; DB 1; Length 498;
Best Local Similarity 71.4%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 XCYWKC 7
   :|||
Db 307 LCYWKAC 313

```

RESULT 6

```

O8E1J1
ID O8E1J1 PRELIMINARY; PRT; 826 AA.
AC O8E1J1
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Periplasmic nitrate reductase.
GN Name=nara; OrderedLocustNames=SC0848;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR-1;
RX MEDLINE=22297666; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Dirkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imprial M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Uterback T.R., McDonald L.A., Feidlyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.,
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123 (2002).
DR EMBL: AE015529; AAN53924.1; -.
DR HSSP: P81166; 2NAP.
DR TIGR: SC0848; -.
DR GO: GO:0005506; F:iron ion binding; IEA.
DR GO: GO:0003015; F:molybdenum ion binding; IEA.
DR GO: GO:0008940; F:nitrate reductase activity; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0042128; F:nitrate assimilation; IEA.
DR InterPro: IPR009010; Asp decarboxylase fold.
DR InterPro: IPR006656; Molybdopecterin.
DR InterPro: IPR006653; Molybdop_Fe4S4.
DR InterPro: IPR006657; Mol_dinuc_bind.
DR InterPro: IPR010051; NAPA.
DR InterPro: IPR006311; Tat.
DR Pfam: PF00384; Molybdop_Fe4S4; 1.
DR Pfam: PF04879; Molybdop_Fe4S4; 1.
DR Pfam: PF01568; Molybdop_Binding; 1.
DR TIGRPFAMs: TIGR01706; NAPA; 1.
DR TIGRPFAMs: TIGR01409; Tat_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 826 AA; 92474 MW; 33474D23868F6316 CRC64;

```

```

Query Match      82.4%; Score 42; DB 2; Length 826;
Best Local Similarity 62.5%; Pred. No. 1,1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 XCYWKC 8
   :|||
Db 473 NCYWTWC 480

```

```

RESULT 7
ID O99GU2 PRELIMINARY; PRT; 192 AA.
AC O99GU2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Helicoverpa armigera nucleopolyhedrovirus G4.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=148363;
[1]
RP SEQUENCE FROM N.A.

```

RA Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
 RT "Sequence analysis of the gp37 gene of Helicobacter armigera single-
 RT nucleocapsid nucleopolyhedrovirus.";
 RU Zhongguo Bing Du Xue 15:35-42(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
 RT "Sequence analysis of the iap3 gene of Helicobacter armigera single-
 RT nucleocapsid nucleopolyhedrovirus.";
 RU Zhongguo Bing Du Xue 15:43-49(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21078302; PubMed=11210934;
 RT "Nucleotide sequence and transcriptional analysis of a putative basic
 RT DNA-binding protein of Helicoverpa armigera polyhedrovirus.";
 RU Virus Genes 22:113-120(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21064569; PubMed=11125177;
 RT Chen X., Idkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
 RA Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
 RT "The sequence of the Helicoverpa armigera single-nucleocapsid
 RT nucleopolyhedrovirus genome.";
 RU J. Gen. Virol. 82:241-257(2001).
 DR EMBL, AF271059; AAG53851.1; -.
 KM Hypothetical protein.
 SQ SEQUENCE 192 AA; 22773 MW; 941387892F8EEDIE CRC64;

Query Match 80.4%; Score 41; DB 2; Length 192;
 Best Local Similarity 71.4%; Pred. No. 43;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
 Db 60 NCHWKVC 66

RESULT 8
 Q9E228 PRELIMINARY; PRT; 192 AA.
 AC Q9E228;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=10468;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Robertson A.P.S.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF275264; AAG17374.1; -.
 KM Hypothetical protein.
 SQ SEQUENCE 192 AA; 22747 MW; D5138789322580B5 CRC64;

Query Match 80.4%; Score 41; DB 2; Length 192;
 Best Local Similarity 71.4%; Pred. No. 43;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
 Db 60 NCHWKVC 66

RESULT 9
 Q91B09 PRELIMINARY; PRT; 192 AA.
 AC Q91B09;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Helicoverpa armigera nuclear polyhedrosis virus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=51313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang C.X., Wu J.C.;
 RT "Genome structure and the p10 gene of the Helicoverpa armigera
 RT nucleopolyhedrovirus.";
 RU Acta Biochim. Biophys. Sin. 33:179-184(2001).
 DR EMBL, AF303045; AAK96351.1; -.
 KM Hypothetical protein.
 SQ SEQUENCE 192 AA; 22745 MW; 94138789371F641E CRC64;

Query Match 80.4%; Score 41; DB 2; Length 192;
 Best Local Similarity 71.4%; Pred. No. 43;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
 Db 60 NCHWKVC 66

RESULT 10
 Q8V505 PRELIMINARY; PRT; 192 AA.
 AC Q8V505;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE ORF11.
 OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=10468;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21830929; PubMed=11842262;
 RT Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F.,
 RA Prensail J.K., Herrmann R., Dolan M., Tingey S., Hu Z.-H., Vlak J.M.;
 RT "Comparative analysis of the complete genome sequences of Helicoverpa
 RT zea and Helicoverpa armigera single-nucleocapsid
 RT nucleopolyhedroviruses.";
 RU J. Gen. Virol. 83:673-684(2002).
 DR EMBL, AF334030; AAL56117.1; -.
 KM Hypothetical protein.
 SQ SEQUENCE 192 AA; 22675 MW; 549DBC848FEEBD CRC64;

Query Match 80.4%; Score 41; DB 2; Length 192;
 Best Local Similarity 71.4%; Pred. No. 43;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
 Db 60 NCHWKVC 66

RESULT 11
 Q83Z37 PRELIMINARY; PRT; 312 AA.
 AC Q83Z37;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein.
 OS Pseudomonas syringae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=317;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR2R;

```
RA Kinschert T.G., Willis D.K.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY253670; AAP14350.1; -.
DR InterPro; IPR011092; DUF1527.
DR Pfam; PF07513; DUF1527; 1.
KW Hypothetical protein.
SQ SEQUENCE 312 AA; 33457 MW; 9C1A00C2B3FAE24 CRC64;

Query Match
Best Local Similarity 80.4%; Score 41; DB 2; Length 312;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 48 ICYWLCT 55

RESULT 12
Q889B2 PRELIMINARY; PRT; 312 AA.
AC Q889B2;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DE Hypothetical protein.
GN OrderedLocustNames=PSPT00849;
OC Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_Taxid=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buehl C.R., Joardar V., Lindeberg M., Sengut J., Paulsen I.T.,
RA Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Deterback T.R., Van Aken S.E., Feldlyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Carlinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarewitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL; AE016858; AA054384.1; -.
DR TIGR; PSPRO849; -.
DR InterPro; IPR011092; DUF1527.
DR Pfam; PF07513; DUF1527; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 312 AA; 33422 MW; 1C91DBDBE3E40F CRC64;

Query Match
Best Local Similarity 80.4%; Score 41; DB 2; Length 312;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 48 ICYWLCT 55

RESULT 13
Q6EVS5 PRELIMINARY; PRT; 317 AA.
AC Q6EVS5;
DT 01-OCT-2004 (TRENBLrel. 28, Created)
DT 01-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein yap154.
GN Name=yap154;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
```

```
OC Enterobacteriaceae; Yersinia.
OX NCBI_Taxid=633;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=32777;
RA Collin F., Billaule A., Mullet C., Simonet M., Marceau M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; A627388; CAF28528.1; -.
KW Hypothetical protein.
SQ SEQUENCE 317 AA; 34498 MW; E3C6914F021AD1AC CRC64;

Query Match
Best Local Similarity 80.4%; Score 41; DB 2; Length 317;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 49 ICYWLCT 56

RESULT 14
Q821I9 PRELIMINARY; PRT; 322 AA.
AC Q821I9;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein STY4576.
GN OrderedLocustNames=STY4576; t4273;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_Taxid=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Doad L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burdand V., Kodoyianni V., Schwartz D.C., Blatterer F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627282; CAD09351.1; -.
DR EMBL; AE016848; AN071731.1; -.
DR InterPro; IPR011092; DUF1527.
DR Pfam; PF07513; DUF1527; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 322 AA; 34841 MW; 8E08C95F19237648 CRC64;

Query Match
Best Local Similarity 80.4%; Score 41; DB 2; Length 322;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 48 ICYWLCT 55
```

RESULT 15

```

Q8YFA7 PRELIMINARY; PRT; 335 AA.
ID Q8YFA7;
AC Q8YFA7;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE TRANSCRIPTIONAL REGULATOR, ARAC FAMILY.
GN OrderedLocustNames=EMW11615;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
RA Delvecchio V.G., Kaputai V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonaki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Leveson J.-J.,
RA Haselkorn R., Kyriides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -! SIMILARITY: Contains 1 HTH arac/xy1s-type DNA-binding domain.
CC EMBL: AE009597; AAL52796.1; -.
DR PIR: A13453; A13453.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006385; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR009057; Homeodomain_like.
DR InterPro: IPR000005; HTHARAC.
DR InterPro: IPR02818; Th1/Pfpr.
DR Pfam: PF01965; Df-1_Pfpr.1.
DR Pfam: PF00165; HTH_ARAC.2.
DR PRINTS: PR00032; HTHARAC.
DR SMART: SM00342; HTH_ARAC.1.
DR PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
KW Complete proteome; DNA-binding; Transcription regulation.
SQ SEQUENCE 335 AA; 37076 MW; F6631F5237F38D6 CRC64;

```

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Query Match 80.4%; Score 41; DB 2; Length 335;
Best Local Similarity 62.5%; Pred. No. 72;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 XCYKVCCT 8
   :|||:
Db 59 RCAMKICT 66

```

Search completed: November 18, 2004, 16:20:53
 Job time : 67 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:40 ; Search time 37 seconds
(without alignments)
20.804 Million cell updates/sec

Title: SEQ1
Perfect score: 51
Sequence: 1 xcywkvct 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	82.4	493	2 JCS486	membrane glycoprot
2	41	80.4	322	2 AF1031	hypothetical prote
3	41	80.4	335	2 A13453	transcription regu
4	41	80.4	3020	2 A43932	mucin 2 precursor
5	40	78.4	475	2 T33943	hypothetical prote
6	38	74.5	381	2 F59101	hypothetical prote
7	38	74.5	1513	2 A54895	mucin 2, intestina
8	38	74.5	1567	2 T00568	hypothetical prote
9	37	72.5	12	1 UOGM2	urotensin II - lon
10	37	72.5	12	2 J50423	urotensin II - A pep
11	37	72.5	12	2 S42765	urotensin II - tel
12	37	72.5	12	2 US0424	urotensin II - B pep
13	37	72.5	13	2 PQ0445	urotensin II - lau
14	37	72.5	83	2 S10706	urotensin II precu
15	37	72.5	125	2 I50499	urotensin II-gamma
16	37	72.5	125	2 I50498	urotensin II-alpha
17	37	72.5	253	2 T47303	hypothetical prote
18	37	72.5	765	2 T09574	transport protein
19	37	72.5	1375	2 T17672	probable DNA repai
20	36	70.6	451	2 F83793	DNA-damage-inducib
21	36	70.6	627	2 B84482	probable gag-prote
22	36	70.6	871	2 S68482	probable membrane
23	36	70.6	1360	2 T12064	DNA binding protei
24	35	68.6	69	2 A86779	hypothetical prote
25	35	68.6	392	2 T46418	hypothetical prote
26	35	68.6	306	2 A40679	transcription enha
27	35	68.6	521	2 T38466	probable NRAMP-fam
28	35	68.6	523	2 B40679	transcription enha
29	35	68.6	654	2 AH2445	hypothetical prote

30	34	66.7	87	2 T33285	hypothetical prote
31	34	66.7	100	2 A31201	Gli-related finger
32	34	66.7	104	2 S69756	hypothetical prote
33	34	66.7	140	2 T33284	hypothetical prote
34	34	66.7	212	2 C87585	hypothetical prote
35	34	66.7	281	2 C82547	hypothetical prote
36	34	66.7	370	2 T47131	G-protein coupled
37	34	66.7	373	2 JCT289	cytochrome d ubiq
38	34	66.7	379	1 B28940	cytochrome d ubiq
39	34	66.7	379	2 A10591	cytochrome d ubiq
40	34	66.7	379	2 A99725	cytochrome d ubiq
41	34	66.7	379	2 B85576	cytochrome d ubiq
42	34	66.7	421	2 T22969	hypothetical prote
43	34	66.7	426	2 T15285	hypothetical prote
44	34	66.7	511	2 A69369	glutamate synthase
45	34	66.7	529	2 C69280	conserved hypothet

ALIGNMENTS

RESULT 1

JCS486 membrane glycoprotein CD30 homolog precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

C/Accession: JCS486

R/Alizawa, S.; Satoh, H.; Horie, R.; Ito, K.; Choi, S.H.; Takeuchi, H.; Watanabe, T.

Gene 182, 155-162, 1996

A/Title: Cloning and characterization of a cDNA for rat CD30 homolog and chromosomal assi

A/Reference number: JCS486; MUID:97136705; PMID:8982082

A/Contents: T cell

A/Molecule type: mRNA

A/Accession: JCS486

A/Residues: 1-493 <Altz>

A/Cross-references: UNIPROT:P97525; DBSP:D42117; NID:G1817523; PIDN:BAA07699.1; PID:d100f

C/Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog

F/1-16/Domain: signal sequence #status predicted <SIG>

F/19-493/Product: membrane glycoprotein CD30 homolog #status predicted <Mat>

F/278-304/Domain: transmembrane #status predicted <TM>

F/305-493/Domain: intracellular #status predicted <INT>

Query Match 82.4%; Score 42; DB 2; Length 493;

Best Local Similarity 71.4%; Pred. No. 22;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKC 7

DB 303 LCVWKC 309

RESULT 2

AF1031 hypothetical protein STY4576 [imported] - Salmonella enterica subsp. enterica serovar Tyf

C/Species: Salmonella enterica subsp. enterica serovar Typh

A/Note: this species has also been called Salmonella typhi

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C/Accession: AF1031

R/Parikh, U.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; MUID:21534947; PMID:1167608

A/Accession: AF1031

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-322 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD09351.1; PID:G16505351; GSPDB:GN00176

C/Genes: STY4576

A/Gene: STY4576

Query Match 80.4% Score 41; DB 2; Length 322;
 Best Local Similarity 62.5% Pred. No. 22;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWVKCT 8
 DB 48 ICYLMVCT 55

RESULT 3

transcription regulator, arag family BMEI1615 [imported] - Brucella melitensis (strain 1

C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: A13453

R:Id:Vechio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: A13453

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-335 <KTR>

A:Cross-references: UNIPROT:Q8YFA7; GB:AE008917; PIDN:AAU52796.1; PID:G17983633; GSPDB:G

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI1615

A:Map position: 1

Query Match 80.4% Score 41; DB 2; Length 335;
 Best Local Similarity 62.5% Pred. No. 23;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWVKCT 8
 DB 59 RCWVKICT 66

RESULT 4

mucin 2 precursor, intestinal - human (fragments)

N:Alternate names: mucin SMWC-41

C:Species: Homo sapiens (man)

C:Date: 10-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C:Accession: A49963; A45106; B45106; A43932; B3353; A61257; PQ0328; PQ0329

R:Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.

J. Biol. Chem. 269, 2440-2446, 1994

A:Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the

A:Reference number: A49963; MUID:94132002; PMID:8300571

A:Accession: A49963

A:Molecule type: mRNA

A:Residues: 1-639 <GU1>

A:Cross-references: UNIPROT:Q02817; UNIPROT:Q14884; GB:I21998

R:Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.W.; Lagace, R.E.; Kim, Y.S.

J. Biol. Chem. 267, 21375-21383, 1992

A:Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstr

A:Reference number: A45106; MUID:93016075; PMID:1400449

A:Accession: A45106

A:Molecule type: mRNA

A:Residues: 626-1895 <GU2>

A:Cross-references: GB:M94132; NID:G186397; PIDN:AAA59164.1; PID:G186398

A:Experimental source: colon

A:Note: Sequence extracted from NCBI backbone (NCBI:116698)

A:Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polymorpi

A:Reference number: A43932; MUID:91358717; PMID:1885763

A:Accession: A43932

A:Molecule type: DNA

A:Residues: 1343-1350, 'U', 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>

A:Cross-references: GB:M74027; NID:G188863; PIDN:AAA59875.1; PID:G188864

A:Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBI:55749; NCBI:55750)

R:Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lampert, D.T.A.; Kim, Y.S.

J. Biol. Chem. 264, 6480-6487, 1989

A:Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and evidence

A:Reference number: A33532; MUID:89197956; PMID:2703501

A:Accession: B33532

A:Molecule type: mRNA

A:Residues: 1916-2193 <GU4>

A:Cross-references: GB:M22405; NID:G188873; PIDN:AAA6334.1; PID:G188874

A:Experimental source: intestine

R:Tany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.

J. Clin. Invest. 87, 77-82, 1991

A:Title: Human bronchus and intestine express the same mucin gene.

A:Reference number: A61257; MUID:91086481; PMID:1985113

A:Accession: A61257

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 'T', 1925-1948, 'TTS', 1952-1954 <JUN>

A:Experimental source: bronchus

R:Xu, G.; Huan, L.; Khatiri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner,

Biochem. Biophys. Res. Commun. 183, 821-828, 1992

A:Title: Human intestinal mucin-like protein (MIP) is homologous with rat MLP in the C-te

A:Reference number: PQ0328; MUID:92198477; PMID:1550588

A:Accession: PQ0328

A:Molecule type: protein

A:Residues: 2328-2468 <XUG>

A:Cross-references: GB:M86523

A:Experimental source: small intestine

A:Accession: PQ0329

A:Molecule type: protein

A:Residues: 2328-2342, 'K', 2344-2354 <XUG1>

C:Genetics:

A:Gene: GDB:MUC2

A:Cross-references: GDB:120203; OMIM:158370

A:Map position: 11p15.5-11p15.5

C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von v

F:2766-2834/Domain: von Willebrand factor type C repeat homology <WVC>

Query Match 80.4% Score 41; DB 2; Length 3020;
 Best Local Similarity 57.1% Pred. No. 1.2e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWVKC 7
 DB 1237 FCYWEIC 1243

RESULT 5

hypothetical protein CO1B4.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T33943

R:Smith, A.; Wamsley, P.; Fronick, W.

submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid CO1B4.

A:Reference number: 221443

A:Accession: T33943

A:Status: preliminary; translated from GB/EMBL/DBDB

A:Molecule type: DNA

A:Residues: 1-475 <SWI>

A:Cross-references: UNIPROT:Q9UAT5; EMBL:AF125352; PIDN:AAU44699.1; GSPDB:GN00023; CESP:G

A:Experimental source: strain Bristol N2; clone CO1B4

C:Genetics:

A:Gene: CESP:CO1B4.7

A:Map position: 5
A:Insertions: 45/2; 80/1; 118/2; 189/3; 239/2; 340/3; 433/3

Query Match 78.4%; Score 40; DB 2; Length 475;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YMKVCT 8
DB 264 YMKICT 269

RESULT 6

F59101
hypothetical protein pX01-86 - Bacillus anthracis virulence plasmid pX01
C:Species: Bacillus anthracis
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C:Accession: F59101
R:Okunaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
J. Bacteriol. 181, 6509-6515, 1999
A:Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harbored
A:Reference number: A59091; MUID:99445483; PMID:10515943
A:Accession: F59101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-581 <OKI>
A:Cross-references: UNIPROT:Q9X356; GB:A0605404; NID:64894216; PID:AA032390.1; PID:9489
A:Experimental source: Strain Sterne
A:Note: similar to hypothetical protein in BLTR-SpoIIIC intergenic region, YX0 B. subtil
C:Genetics:
A:Gene: pX01-86
A:Genome: plasmid

Query Match 74.5%; Score 38; DB 2; Length 381;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YMKVCT 8
DB 340 YMKICT 345

RESULT 7

A54895
mucin 2, intestinal/tracheal - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C:Accession: A54895
R:Ohmori, H.; Dohman, A.F.; Gallup, M.; Tsuda, T.; Kai, H.; Gum Jr., J.R.; Kim, Y.S.; B
J. Biol. Chem. 269, 17833-17840, 1994
A:Title: Molecular cloning of the amino-terminal region of a rat MUC 2 mucin gene homolog
A:Reference number: A54895; MUID:94299489; PMID:8027037
A:Accession: A54895
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1513 <OHM>
A:Cross-references: UNIPROT:Q62635; GB:U07615
C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
C:Keywords: intestine

Query Match 74.5%; Score 38; DB 2; Length 1513;
Best Local Similarity 57.1%; Pred. No. 21e-02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
DB 1234 FCTWCTC 1240

RESULT 8

T00568
hypothetical protein At2g39580 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F12L6.24

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00568; B84819

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence.
A:Reference number: Z14168
A:Accession: T00568

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1567 <ROU>

A:Cross-references: UNIPROT:Q80645; EMBL:AC004218; NID:93355463; PID:93355487
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.;
eues, D.; Niernan, M.C.; White, O.; Eiken, U.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84819

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1567 <STO>

A:Cross-references: GB:A8002093; NID:93355487; PID:AA027849.1; GSPDB:GND0139
C:Genetics:
A:Gene: At2g39580; F12L6.24
A:Map position: 2

A:Insertions: 306/1; 346/3; 395/3; 688/1; 843/1; 945/3; 991/3; 1098/1
C:Superfamily: Arabidopsis thaliana hypothetical protein F12L6.24

Query Match 74.5%; Score 38; DB 2; Length 1567;
Best Local Similarity 57.1%; Pred. No. 2.2e-02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
DB 1538 RCTWSLC 1544

RESULT 9

U00GM2
urotensin II - long-jawed mudsucker
C:Species: Gallitichthys mirabilis (long-jawed mudsucker)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C:Accession: A01409
R:Pearson, D.; Shively, J.E.; Clark, B.R.; Geschwind, I.I.; Barkley, M.; Nishioka, R.; B
Proc. Natl. Acad. Sci. U.S.A. 77, 5021-5024, 1980
A:Title: Urotensin II: a somatostatin-like peptide in the caudal neurosecretory system o
A:Reference number: A01409; MUID:81054904; PMID:6107911
A:Accession: A01409

A:Molecule type: protein
A:Residues: 1-12 <PEA>
A:Cross-references: UNIPROT:P01147
A:Note: the proposed sequence was confirmed by synthesis of a peptide with the same struc
C:Comment: Urotensin II is found in the teleost caudal neurosecretory system and is invo
C:Superfamily: urotensin II
C:Keywords: neuropeptide, osmoregulation
F:6-11/Disulfide bonds: #status experimental

Query Match 72.5%; Score 37; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 7.7;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVC 7
DB 5 DCFWKYC 11

RESULT 10

U00423
urotensin II-A peptide - white sucker
C:Species: Catostomus commersoni (white sucker)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

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Thu Nov 18 16:38:25 2004

seq1.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 16:19:40 ; Search time 139 Seconds
(without alignments)

20.381 Million cell updates/sec

Title: SEQ1
Perfect score: 51
Sequence: 1 xcywkvct 8

Scoring table: BLASTN62DX
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	92.2	8	9 US-09-781-980-6	Sequence 22, Appl1
2	47	92.2	9	16 US-10-427-160A-22	Sequence 66, Appl1
3	47	92.2	9	17 US-10-444-853A-515	Sequence 515, Appl1
4	47	92.2	14	16 US-10-258-766A-1	Sequence 1, Appl1
5	47	92.2	14	16 US-10-258-766A-6	Sequence 6, Appl1
6	47	92.2	14	16 US-10-258-766A-7	Sequence 7, Appl1
7	47	92.2	14	16 US-10-258-766A-8	Sequence 8, Appl1
8	47	92.2	14	16 US-10-258-766A-13	Sequence 13, Appl1
9	47	92.2	14	16 US-10-258-766A-14	Sequence 14, Appl1
10	46	90.2	7	16 US-10-258-766A-5	Sequence 5, Appl1
11	46	90.2	7	16 US-10-258-766A-10	Sequence 10, Appl1
12	46	90.2	7	16 US-10-258-766A-12	Sequence 12, Appl1
13	46	90.2	9	13 US-10-036-869-13	Sequence 13, Appl1

14	46	90.2	33	14 US-10-300-083-3	Sequence 3, Appl1
15	46	90.2	34	13 US-10-036-869-15	Sequence 15, Appl1
16	43	84.3	8	9 US-09-781-980-5	Sequence 5, Appl1
17	42	82.4	27	14 US-10-058-053A-263	Sequence 263, Appl1
18	42	82.4	27	16 US-10-838-226-263	Sequence 263, Appl1
19	42	82.4	78	14 US-10-058-053A-38	Sequence 38, Appl1
20	42	82.4	78	14 US-10-058-053A-212	Sequence 212, Appl1
21	42	82.4	78	16 US-10-838-226-38	Sequence 38, Appl1
22	42	82.4	78	16 US-10-838-226-212	Sequence 212, Appl1
23	42	82.4	275	16 US-10-322-596-153	Sequence 153, Appl1
24	41	80.4	21	14 US-10-058-053A-234	Sequence 234, Appl1
25	41	80.4	21	16 US-10-838-226-234	Sequence 234, Appl1
26	41	80.4	40	14 US-10-058-053A-231	Sequence 231, Appl1
27	41	80.4	40	14 US-10-058-053A-264	Sequence 264, Appl1
28	41	80.4	40	16 US-10-838-226-231	Sequence 231, Appl1
29	41	80.4	40	16 US-10-838-226-264	Sequence 264, Appl1
30	41	80.4	45	16 US-10-058-053A-280	Sequence 280, Appl1
31	41	80.4	45	16 US-10-838-226-280	Sequence 280, Appl1
32	41	80.4	90	14 US-10-058-053A-80	Sequence 80, Appl1
33	41	80.4	90	16 US-10-838-226-80	Sequence 80, Appl1
34	41	80.4	93	14 US-10-058-053A-116	Sequence 116, Appl1
35	41	80.4	93	16 US-10-838-226-116	Sequence 116, Appl1
36	41	80.4	95	14 US-10-058-053A-89	Sequence 89, Appl1
37	41	80.4	95	16 US-10-838-226-89	Sequence 89, Appl1
38	41	80.4	302	16 US-10-437-963-152285	Sequence 152285, Appl1
39	41	80.4	5179	9 US-09-922-217-1068	Sequence 1068, Appl1
40	41	80.4	5179	13 US-09-833-263-1068	Sequence 1068, Appl1
41	41	80.4	5179	13 US-10-025-380-1068	Sequence 1068, Appl1
42	41	80.4	5179	16 US-10-734-384-121	Sequence 121, Appl1
43	40	78.4	54	15 US-10-424-599-254495	Sequence 254495, Appl1
44	40	78.4	62	15 US-10-424-599-212336	Sequence 212336, Appl1
45	39	76.5	77	15 US-10-424-599-218190	Sequence 218190, Appl1

ALIGNMENTS

RESULT 1
US-09-781-980-6
Sequence 6, Application US/09781980
Publication No. US20010029035A1
GENERAL INFORMATION:
APPLICANT: EISENHUT, MICHAEL
APPLICANT: MIER, WALTER
APPLICANT: ERITJA, RAMON
APPLICANT: HABERKORN, UWE
TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
FILE REFERENCE: 2502498.991110
CURRENT APPLICATION NUMBER: US/09/781, 980
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: DE 100 06 572
PRIOR FILING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-781-980-6
Query Match 92.2% ; Score 47 ; DB 9 ; Length 8 ;
Best Local Similarity 75.0% ; Pred. No. 1.4e-06 ;
Matches 6 ; Conservative 1 ; Mismatches 1 ; Gaps 0 ;

RESULT 2

US-10-427-160A-22

; Sequence 22, Application US/10427160A

; Publication No. US20040110296A1

; GENERAL INFORMATION:

; APPLICANT: Sirta Therapeutics, Inc.

; APPLICANT: Vargese, Chandra

; APPLICANT: Haeblerli, Peter

; APPLICANT: Wang, Weimin

; APPLICANT: Cheng, Tongqian

; TITLE OF INVENTION: Conjugates and Compositions for Cellular Delivery

; FILE REFERENCE: 600/032 (MBH02-312-A)

; CURRENT APPLICATION NUMBER: US/10/427,160A

; CURRENT FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: PCT/US 02/15876

; PRIOR FILING DATE: 2002-05-17

; PRIOR APPLICATION NUMBER: US 60/292,217

; PRIOR FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: US 60/362,016

; PRIOR FILING DATE: 2002-03-06

; PRIOR APPLICATION NUMBER: US 60/306,883

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/311,865

; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: PCT/US 03/05346

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT/US 03/05028

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 22

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: Ser stands for optional Serine for coupling

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (2)..(2)

; OTHER INFORMATION: Phe stands for optional D isomer for stability

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; NAME/KEY: misc_feature

; LOCATION: (5)..(5)

; OTHER INFORMATION: Trp stands for optional D isomer for stability

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (5)..(5)

; OTHER INFORMATION: TTP stands for optional D isomer for stability

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; LOCATION: (5)..(5)

; OTHER INFORMATION: TTP stands for optional D isomer for stability

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; NAME/KEY: misc_feature

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; LOCATION: (5)..(5)

; OTHER INFORMATION: TTP stands for optional D isomer for stability

; FEATURE:

; APPLICANT: McSwigen, James

; APPLICANT: Beigelman, Leonid

; APPLICANT: Macejak, Dennis

; APPLICANT: Zinnen, Shawn

; APPLICANT: Pavo, Pamela

; APPLICANT: Morrissey, David

; APPLICANT: Fornaugh, Kathy

; APPLICANT: Mokier, Victor

; APPLICANT: Jamison, Shaon

; APPLICANT: Walsh, Nereenda

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using

; FILE REFERENCE: 400/114 (MBH03-465)

; CURRENT APPLICATION NUMBER: US/10/444,853A

; CURRENT FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: US 10/417,012

; PRIOR FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: PCT/US03/05346

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT/US03/05028

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: US 60/409,293

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: US 60/440,129

; PRIOR FILING DATE: 2003-01-15

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 626

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 515

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)..(1)

; OTHER INFORMATION: Somatostatin (tyr-3-octreotate)

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (2)..(2)

; OTHER INFORMATION: Phe at position 2 is optionally the D-isomer.

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (5)..(5)

; OTHER INFORMATION: TTP at position 5 is optionally the D-isomer.

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (5)..(5)

; OTHER INFORMATION: TTP at position 5 is optionally the D-isomer.

; FEATURE:

; NAME/KEY: MISC FEATURE

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; OTHER INFORMATION: TTP at position 5 is optionally the D-isomer.

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; LOCATION: (5)..(5)

; OTHER INFORMATION: TTP at position 5 is optionally the D-isomer.

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (5)..(5)

; OTHER INFORMATION: TTP at position 5 is optionally the D-isomer.

US-10-444-853A-515

Sequence 515, Application US/10444853A

Publication No. US20040192626A1

GENERAL INFORMATION:

APPLICANT: Sirta Therapeutics, Inc.

APPLICANT: Haeblerli, Peter

Query Match 92.2%; Score 47; DB 16; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8

DB 2 FCYWKTC 9

RESULT 3

US-10-444-853A-515

Sequence 515, Application US/10444853A

Publication No. US20040192626A1

GENERAL INFORMATION:

APPLICANT: Sirta Therapeutics, Inc.

APPLICANT: Haeblerli, Peter

Query Match 92.2%; Score 47; DB 17; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8

DB 2 FCYWKTC 9

RESULT 4

US-10-258-766A-1

Sequence 1, Application US/10258766A

Publication No. US20040136907A1

GENERAL INFORMATION:

APPLICANT: Biosynthema, Inc.

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/ TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
/ FILE REFERENCE: 717816.17
/ CURRENT APPLICATION NUMBER: US/10/258,766A
/ CURRENT FILING DATE: 2002-10-25
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
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/ LOCATION: (1)..(1)
/ OTHER INFORMATION: Arg(Pmc)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Asp(OtBu)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Dtyr(OtBu)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Asp(beta-OAl1)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (6)..(6)
/ OTHER INFORMATION: Lys(Mtc)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (7)..(7)
/ OTHER INFORMATION: Dphe
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (8)..(8)
/ OTHER INFORMATION: Cys(Acm)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (9)..(9)
/ OTHER INFORMATION: Tyr(OtBu)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (10)..(10)
/ OTHER INFORMATION: Dtip(tBoc)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (11)..(11)
/ OTHER INFORMATION: Lys(tBoc)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (12)..(12)
/ OTHER INFORMATION: Thr(OtBu)
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (13)..(13)
/ OTHER INFORMATION: Cys(Acm)
/ NAME/KEY: MOD_RES
/ LOCATION: (14)..(14)
/ OTHER INFORMATION: Thr(OtBu)-O-RESIN
US-10-258-766A-1

```

```

Query Match      92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 XCYWKVCT 8
       :|||||
Db      7 FCYWKVCT 14

```

```

RESULT 5
US-10-258-766A-6
/ Sequence 6, Application US/10258766A
/ Publication No. US20040136907A1
/ GENERAL INFORMATION:
/ APPLICANT: Biosynthema, Inc.
/ TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
/ FILE REFERENCE: 717816.17
/ CURRENT APPLICATION NUMBER: US/10/258,766A
/ CURRENT FILING DATE: 2002-10-25
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: DISULFID
/ LOCATION: (8)..(13)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(5)
/ OTHER INFORMATION: Amide bond between residues 1 and 5
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Dtyr
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (7)..(7)
/ OTHER INFORMATION: Dphe
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (10)..(10)
/ OTHER INFORMATION: Dtip
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (14)..(14)
/ OTHER INFORMATION: Thr-OH
US-10-258-766A-6

```

```

Query Match      92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 XCYWKVCT 8
       :|||||
Db      7 FCYWKVCT 14

```

```

RESULT 6
US-10-258-766A-7
/ Sequence 7, Application US/10258766A
/ Publication No. US20040136907A1
/ GENERAL INFORMATION:
/ APPLICANT: Biosynthema, Inc.
/ TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
/ FILE REFERENCE: 717816.17
/ CURRENT APPLICATION NUMBER: US/10/258,766A
/ CURRENT FILING DATE: 2002-10-25
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: DISULFID
/ LOCATION: (8)..(13)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: MISC FEATURE

```

LOCATION: (1)..(5)
OTHER INFORMATION: Amide bond between residues 1 and 5
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: DTYr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)..(6)
OTHER INFORMATION: NH-DTPA
OTHER INFORMATION: Lys
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: DpHe
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (10)..(10)
OTHER INFORMATION: DTrp
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (14)..(14)
OTHER INFORMATION: Thr-OH
US-10-258-766A-7

Query Match 92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 7 FCYWKTCCT 14

RESULT 7
US-10-258-766A-8
Sequence 8, Application US/10258766A
Publication No. US20040136907A1
GENERAL INFORMATION:
APPLICANT: Biosynthema, Inc.
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
FILE REFERENCE: 717816.17
CURRENT APPLICATION NUMBER: US/10/258,766A
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: Arg(Pmc)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: DTYr(OcBu)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)..(5)
OTHER INFORMATION: Asp(beta-OAl1)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)..(6)
OTHER INFORMATION: Lys(Mct)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: DpHe
FEATURE:
NAME/KEY: MOD_RES
NAME/KEY: MOD_RES

LOCATION: (8)..(8)
OTHER INFORMATION: Cys(Acm)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (9)..(9)
OTHER INFORMATION: TYr(OcBu)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (10)..(10)
OTHER INFORMATION: DTrp(tBoc)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (11)..(11)
OTHER INFORMATION: Lys(tBoc)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (12)..(12)
OTHER INFORMATION: Thr(OcBu)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (13)..(13)
OTHER INFORMATION: Cys(Acm)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (14)..(14)
OTHER INFORMATION: Thr(Ol)(OcBu)-O-RESIN
US-10-258-766A-8

Query Match 92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
DB 7 FCYWKTCCT 14

RESULT 8
US-10-258-766A-13
Sequence 13, Application US/10258766A
Publication No. US20040136907A1
GENERAL INFORMATION:
APPLICANT: Biosynthema, Inc.
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
FILE REFERENCE: 717816.17
CURRENT APPLICATION NUMBER: US/10/258,766A
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: DTYr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: DpHe
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (10)..(10)
OTHER INFORMATION: DTrp
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (14)..(14)
OTHER INFORMATION: Thr(Ol)-OH
FEATURE:
NAME/KEY: DISULFID
LOCATION: (8)..(13)
OTHER INFORMATION:

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Page 5

FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(5)
OTHER INFORMATION: Amide bond between residues 1 and 5
US-10-258-766A-13

Query Match 92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
:|||||
Db 7 FCYWKTCCT 14

RESULT 9
US-10-258-766A-14
Sequence 14, Application US/10258766A
Publication No. US20040136907A1
GENERAL INFORMATION:
APPLICANT: Biosynthema, Inc.
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
FILE REFERENCE: 717816.17
CURRENT APPLICATION NUMBER: US/10/258,766A
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: DTYr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)..(6)
OTHER INFORMATION: NH-DTPA
OTHER INFORMATION: |
OTHER INFORMATION: Lys
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: DPhe
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (10)..(10)
OTHER INFORMATION: DTrp
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (14)..(14)
OTHER INFORMATION: Thr(Ol)-OH
FEATURE:
NAME/KEY: DISULFID
LOCATION: (8)..(13)
OTHER INFORMATION:
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(5)
OTHER INFORMATION: Amide bond between residues 1 and 5
US-10-258-766A-14

Query Match 92.2%; Score 47; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 XCYWKVCT 8
:|||||
Db 7 FCYWKTCCT 14

RESULT 10

US-10-258-766A-5
Sequence 5, Application US/10258766A
Publication No. US20040136907A1
GENERAL INFORMATION:
APPLICANT: Biosynthema, Inc.
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
FILE REFERENCE: 717816.17
CURRENT APPLICATION NUMBER: US/10/258,766A
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DISULFID
LOCATION: (1)..(6)
OTHER INFORMATION:
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: Cys(Acm)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (2)..(2)
OTHER INFORMATION: Tyr(OlBu)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (3)..(3)
OTHER INFORMATION: DTrp(tBoc)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: Lys(tBoc)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)..(5)
OTHER INFORMATION: Thr(OlBu)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)..(6)
OTHER INFORMATION: Cys(Acm)
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION:
US-10-258-766A-5

Query Match 90.2%; Score 46; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYWKVCT 8
:|||||
Db 1 CYWKTCCT 7

RESULT 11
US-10-258-766A-10
Sequence 10, Application US/10258766A
Publication No. US20040136907A1
GENERAL INFORMATION:
APPLICANT: Biosynthema, Inc.
TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
FILE REFERENCE: 717816.17
CURRENT APPLICATION NUMBER: US/10/258,766A
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 7
TYPE: PRT

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ORGANISM: Homo sapiens
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (1)..(1)
  OTHER INFORMATION: Cys (Acm)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (2)..(2)
  OTHER INFORMATION: Tyr (OCBu)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (3)..(3)
  OTHER INFORMATION: DTrp (tBoc)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (4)..(4)
  OTHER INFORMATION: Lys (tBoc)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (5)..(5)
  OTHER INFORMATION: Thr (OCBu)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (6)..(6)
  OTHER INFORMATION: Cys (Acm)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (7)..(7)
  OTHER INFORMATION: Thr (OL) (OCBu) -O-RESIN
US-10-258-766A-10
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Query Match 90.2%; Score 46; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYWKTCT 8
DB 1 CYWKTCT 7

RESULT 12

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US-10-258-766A-12
Sequence 12, Application US/10258766A
Publication No. US20040136907A1
GENERAL INFORMATION:
  APPLICANT: Biosynhema, Inc.
  TITLE OF INVENTION: RGD (ARG-GLY-ASP) COUPLED TO (NEURO) PEPTIDES
  FILE REFERENCE: 717816.17
  CURRENT APPLICATION NUMBER: US/10/258,766A
  CURRENT FILING DATE: 2002-10-25
  NUMBER OF SEQ ID NOS: 14
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 12
  LENGTH: 7
  TYPE: PRT
  ORGANISM: Homo sapiens
FEATURE:
  NAME/KEY: DISULFID
  LOCATION: (1)..(6)
  OTHER INFORMATION:
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (1)..(1)
  OTHER INFORMATION: Cys (Acm)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (2)..(2)
  OTHER INFORMATION: Tyr (OCBu)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (3)..(3)
  OTHER INFORMATION: DTrp (tBoc)
FEATURE:
```

```
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: Lys (tBoc)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (5)..(5)
  OTHER INFORMATION: Thr (OCBu)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (6)..(6)
  OTHER INFORMATION: Cys (Acm)
FEATURE:
  NAME/KEY: MOD_RES
  LOCATION: (7)..(7)
  OTHER INFORMATION: Thr (OL) (OCBu) -O-RESIN
US-10-258-766A-12
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Query Match 90.2%; Score 46; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CYWKTCT 8
DB 1 CYWKTCT 7

RESULT 13

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US-10-036-869-13
Sequence 13, Application US/10036869
Publication No. US20020151516A1
GENERAL INFORMATION:
  APPLICANT: Mixson, James A
  TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
  THERAPY
  NUMBER OF SEQUENCES: 43
  CORRESPONDENCE ADDRESS:
  ADDRESS: Connelly, Bove, Lodge, & Hutz
  STREET: 1220 Market Street, P.O. Box 2207
  CITY: Wilmington
  STATE: Delaware
  COUNTRY: U.S.A.
  ZIP: 19899
  COMPUTER READABLE FORM:
  MEDIUM TYPE: floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/036,869
  FILING DATE: 29-No. US20020151516A1-2001
  CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/385,526
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US 08/608,845
  FILING DATE: 16-JUL-1996
  ATTORNEY/AGENT INFORMATION:
  NAME: McMorris Jr., Robert G
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (302) 658-9141
  TELEFAX: (302) 658-5613
  INFORMATION FOR SEQ ID NO: 13:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 9 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-036-869-13
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Query Match 90.2%; Score 46; DB 13; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 XCYWKC 7
:|||||
Db 2 FCYWKC 8

RESULT 14
US-10-300-083-3

; Sequence 3, Application US/10300083
; Publication No. US20030153502A1

; GENERAL INFORMATION:

; APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA
; TITLE OF INVENTION: SYNTHETIC APPROACH TO DESIGNED CHEMICAL
; STRUCTURES

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: MEETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
; STREET: 119 No. US20030153502A1th Fourth Street, Suite 203
; City: Minneapolis
; STATE: Minnesota
; COUNTRY: U.S.A.
; ZIP: 55401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/300,083
; FILING DATE: 20-No. US20030153502A1-2002
; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/09/194,296
; FILING DATE: 15-Oct-1999

; APPLICATION NUMBER: US 08/653,632
; FILING DATE: 24-MAY-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: MCCORMACK, MYRA M.
; REGISTRATION NUMBER: 36,602

; REFERENCE/DOCKET NUMBER: 110,0030220
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-305-1225
; TELEFAX: 612-305-1228

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; MOLECULE TYPE: peptide
; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-300-083-3

Query Match 90.2%; Score 46; DB 14; Length 33;
Best Local Similarity 85.7%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKC 7
:|||||
Db 12 FCYWKC 18

RESULT 15
US-10-036-869-15

; Sequence 15, Application US/10036869
; Publication No. US20020151516A1

; GENERAL INFORMATION:

; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER DNA COMPLEXES CONTAINING DNA
; ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; THERAPY

; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/036,869
; FILING DATE: 29-No. US20020151516A1-2001
; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,526
; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: McMorow Jr., Robert G
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 658-5613
; TELEFAX: (302) 658-5613

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-036-869-15

Query Match 90.2%; Score 46; DB 13; Length 34;
Best Local Similarity 85.7%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XCYWKC 7
:|||||
Db 2 FCYWKC 8

Search completed: November 18, 2004, 16:24:58
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Legal Date: 10-14-2004

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Total number of pages: 44

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